

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/584,362
Source: IFWP
Date Processed by STIC: 7/7/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 07/07/2006

PATENT APPLICATION: US/10/584,362

TIME: 14:37:38

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\07072006\J584362.raw

```

4 <110> APPLICANT: Bos, Martine Petronella
5      Poolman, Jan
6      Tefsen, Boris
7      Tommassen, Johannes Petrus Maria
9 <120> TITLE OF INVENTION: Vaccine
12 <130> FILE REFERENCE: VB60639
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/584,362
15 <141> CURRENT FILING DATE: 2006-06-23
17 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/014770
18 <151> PRIOR FILING DATE: 2004-12-21
20 <150> PRIOR APPLICATION NUMBER: GB 0329837.0
21 <151> PRIOR FILING DATE: 2003-12-23
23 <150> PRIOR APPLICATION NUMBER: GB0416398.6
24 <151> PRIOR FILING DATE: 2004-07-22
26 <160> NUMBER OF SEQ ID NOS: 27
28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 20
32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
35 <220> FEATURE:
36 <223> OTHER INFORMATION: Primer
38 <400> SEQUENCE: 1
39 cccaaagcga agtgggtcgaa                                20
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 26
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial Sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: Primer
49 <400> SEQUENCE: 2
50 gtcgactatc ggtagggcgg gaactg                            26
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 26
54 <212> TYPE: DNA
55 <213> ORGANISM: Artificial Sequence
57 <220> FEATURE:
58 <223> OTHER INFORMATION: Primer
60 <400> SEQUENCE: 3
61 gtcgacgacc gcatcatcgt gatgga                            26
63 <210> SEQ ID NO: 4
64 <211> LENGTH: 20
65 <212> TYPE: DNA

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66 <213> ORGANISM: Artificial Sequence
68 <220> FEATURE:
69 <223> OTHER INFORMATION: Primer
71 <400> SEQUENCE: 4
72 ttcgtcgctg ccgacctgtt                20
74 <210> SEQ ID NO: 5
75 <211> LENGTH: 28
76 <212> TYPE: DNA
77 <213> ORGANISM: Artificial Sequence
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Primer
82 <400> SEQUENCE: 5
83 ttcatatgat agaaaaactg acttttcgg      28
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 27
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Primer
93 <400> SEQUENCE: 6
94 gacgtcccat ttcggacggc attttgt      27
96 <210> SEQ ID NO: 7
97 <211> LENGTH: 31
98 <212> TYPE: PRT
99 <213> ORGANISM: Neisseria meningitidis
101 <400> SEQUENCE: 7
102 Arg His Ala Asn Val Gly Arg Asn Ala Phe Glu Leu Phe Leu Ile Gly
103   1          5          10          15
104 Ser Gly Ser Asp Gln Ala Lys Gly Thr Asp Pro Leu Lys Asn His
105   20          25          30
108 <210> SEQ ID NO: 8
109 <211> LENGTH: 29
110 <212> TYPE: PRT
111 <213> ORGANISM: Neisseria meningitidis
113 <400> SEQUENCE: 8
114 Lys Gly Lys Asn Pro Asp Glu Leu Ala Tyr Leu Ala Gly Asp Gln Lys
115   1          5          10          15
116 Arg Tyr Ser Thr Lys Arg Ala Ser Ser Ser Trp Ser Thr
117   20          25
120 <210> SEQ ID NO: 9
121 <211> LENGTH: 27
122 <212> TYPE: PRT
123 <213> ORGANISM: Neisseria meningitidis
125 <400> SEQUENCE: 9
126 Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr
127   1          5          10          15
128 Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala
129   20          25
132 <210> SEQ ID NO: 10

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133 <211> LENGTH: 28
134 <212> TYPE: PRT
135 <213> ORGANISM: Neisseria meningitidis
137 <400> SEQUENCE: 10
138 Ala Arg Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp
139 1 5 10 15
140 Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly Val Leu
141 20 25
144 <210> SEQ ID NO: 11
145 <211> LENGTH: 20
146 <212> TYPE: DNA
147 <213> ORGANISM: Artificial Sequence
149 <220> FEATURE:
150 <223> OTHER INFORMATION: Primer
152 <400> SEQUENCE: 11
153 atgcctgcaa ccttcaagtg 20
155 <210> SEQ ID NO: 12
156 <211> LENGTH: 30
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <223> OTHER INFORMATION: Primer
163 <400> SEQUENCE: 12
164 atgtcgacaa tcgcccctca agtcggtttg 30
166 <210> SEQ ID NO: 13
167 <211> LENGTH: 28
168 <212> TYPE: DNA
169 <213> ORGANISM: Artificial Sequence
171 <220> FEATURE:
172 <223> OTHER INFORMATION: Primer
174 <400> SEQUENCE: 13
175 atgtcgacta cctgcggccg gattatgc 28
177 <210> SEQ ID NO: 14
178 <211> LENGTH: 32
179 <212> TYPE: DNA
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Primer
185 <400> SEQUENCE: 14
186 atgacgtctc agggtcgttt gttgcgtccg gc 32
188 <210> SEQ ID NO: 15
189 <211> LENGTH: 30
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Primer
196 <400> SEQUENCE: 15
197 agcgtcgact tcagacggcc acgttgtgtc 30
199 <210> SEQ ID NO: 16

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```

200 <211> LENGTH: 27
201 <212> TYPE: DNA
202 <213> ORGANISM: Artificial Sequence
204 <220> FEATURE:
205 <223> OTHER INFORMATION: Primer
207 <400> SEQUENCE: 16
208 agcgtcgacg ctgaggtctg cctcgtg          27
210 <210> SEQ ID NO: 17
211 <211> LENGTH: 31
212 <212> TYPE: DNA
213 <213> ORGANISM: Artificial Sequence
215 <220> FEATURE:
216 <223> OTHER INFORMATION: Primer
218 <400> SEQUENCE: 17
219 atcatatggc tcgtttatTT tcaactcaaac c      31
221 <210> SEQ ID NO: 18
222 <211> LENGTH: 26
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Primer
229 <400> SEQUENCE: 18
230 tgcatatgga tgccgttgcg gcggag          26
232 <210> SEQ ID NO: 19
233 <211> LENGTH: 29
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Primer
240 <400> SEQUENCE: 19
241 tgggatcctc agggtcgttt gttgcgtcc      29
243 <210> SEQ ID NO: 20
244 <211> LENGTH: 802
245 <212> TYPE: PRT
246 <213> ORGANISM: Neisseria meningitidis
248 <400> SEQUENCE: 20
249 Leu Ala Arg Leu Phe Ser Leu Lys Pro Leu Val Leu Ala Leu Gly Leu
250 1          5          10          15
251 Cys Phe Gly Thr His Cys Ala Ala Asp Ala Val Ala Ala Glu Glu
252          20          25          30
253 Thr Asp Asn Pro Thr Ala Gly Glu Ser Val Arg Ser Val Ser Glu Pro
254          35          40          45
255 Ile Gln Pro Thr Ser Leu Ser Leu Gly Ser Thr Cys Leu Phe Cys Ser
256          50          55          60
257 Asn Glu Ser Gly Ser Pro Glu Arg Thr Glu Ala Ala Val Gln Gly Ser
258 65          70          75          80
259 Gly Glu Ala Ser Ile Pro Glu Asp Tyr Thr Arg Ile Val Ala Asp Arg
260          85          90          95
261 Met Glu Gly Gln Ser Gln Val Gln Val Arg Ala Glu Gly Asn Val Val

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262				100				105				110				
263	Val	Glu	Arg	Asn	Arg	Thr	Thr	Leu	Asn	Thr	Asp	Trp	Ala	Asp	Tyr	Asp
264				115				120					125			
265	Gln	Ser	Gly	Asp	Thr	Val	Thr	Ala	Gly	Asp	Arg	Phe	Ala	Leu	Gln	Gln
266				130				135				140				
267	Asp	Gly	Thr	Leu	Ile	Arg	Gly	Glu	Thr	Leu	Thr	Tyr	Asn	Leu	Glu	Gln
268	145						150				155					160
269	Gln	Thr	Gly	Glu	Ala	His	Asn	Val	Arg	Met	Glu	Ile	Glu	Gln	Gly	Gly
270					165					170					175	
271	Arg	Arg	Leu	Gln	Ser	Val	Ser	Arg	Thr	Ala	Glu	Met	Leu	Gly	Glu	Gly
272				180					185					190		
273	His	Tyr	Lys	Leu	Thr	Glu	Thr	Gln	Phe	Asn	Thr	Cys	Ser	Ala	Gly	Asp
274				195				200					205			
275	Ala	Gly	Trp	Tyr	Val	Lys	Ala	Ala	Ser	Val	Glu	Ala	Asp	Arg	Glu	Lys
276				210				215				220				
277	Gly	Ile	Gly	Val	Ala	Lys	His	Ala	Ala	Phe	Val	Phe	Gly	Gly	Val	Pro
278	225					230				235						240
279	Ile	Phe	Tyr	Thr	Pro	Trp	Ala	Asp	Phe	Pro	Leu	Asp	Gly	Asn	Arg	Lys
280					245					250					255	
281	Ser	Gly	Leu	Leu	Val	Pro	Ser	Leu	Ser	Ala	Gly	Ser	Asp	Gly	Val	Ser
282				260					265					270		
283	Leu	Ser	Val	Pro	Tyr	Tyr	Phe	Asn	Leu	Ala	Pro	Asn	Leu	Asp	Ala	Thr
284				275				280					285			
285	Phe	Ala	Pro	Ser	Val	Ile	Gly	Glu	Arg	Gly	Ala	Val	Phe	Asp	Gly	Gln
286				290			295				300					
287	Val	Arg	Tyr	Leu	Arg	Pro	Asp	Tyr	Ala	Gly	Gln	Ser	Asp	Leu	Thr	Trp
288	305					310				315						320
289	Leu	Pro	His	Asp	Lys	Lys	Ser	Gly	Arg	Asn	Asn	Arg	Tyr	Gln	Ala	Lys
290					325					330					335	
291	Trp	Gln	His	Arg	His	Asp	Ile	Ser	Asp	Thr	Leu	Gln	Ala	Gly	Val	Asp
292				340					345					350		
293	Phe	Asn	Gln	Val	Ser	Asp	Ser	Gly	Tyr	Tyr	Arg	Asp	Phe	Tyr	Gly	Asn
294				355				360					365			
295	Lys	Glu	Ile	Ala	Gly	Asn	Val	Asn	Leu	Asn	Arg	Arg	Val	Trp	Leu	Asp
296				370			375				380					
297	Tyr	Gly	Gly	Arg	Ala	Ala	Gly	Gly	Ser	Leu	Asn	Ala	Gly	Leu	Ser	Val
298	385					390					395					400
299	Leu	Lys	Tyr	Gln	Thr	Leu	Ala	Asn	Gln	Ser	Gly	Tyr	Lys	Asp	Lys	Pro
300					405					410					415	
301	Tyr	Ala	Leu	Met	Pro	Arg	Leu	Ser	Val	Glu	Trp	Arg	Lys	Asn	Thr	Gly
302				420					425					430		
303	Arg	Ala	Gln	Ile	Gly	Val	Ser	Ala	Gln	Phe	Thr	Arg	Phe	Ser	His	Asp
304				435				440					445			
305	Ser	Arg	Gln	Asp	Gly	Ser	Arg	Leu	Val	Val	Tyr	Pro	Asp	Ile	Lys	Trp
306				450			455					460				
307	Asp	Phe	Ser	Asn	Ser	Trp	Gly	Tyr	Val	Arg	Pro	Lys	Leu	Gly	Leu	His
308	465					470					475					480
309	Ala	Thr	Tyr	Tyr	Ser	Leu	Asn	Arg	Phe	Gly	Ser	Gln	Glu	Ala	Arg	Arg
310					485					490					495	

VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number